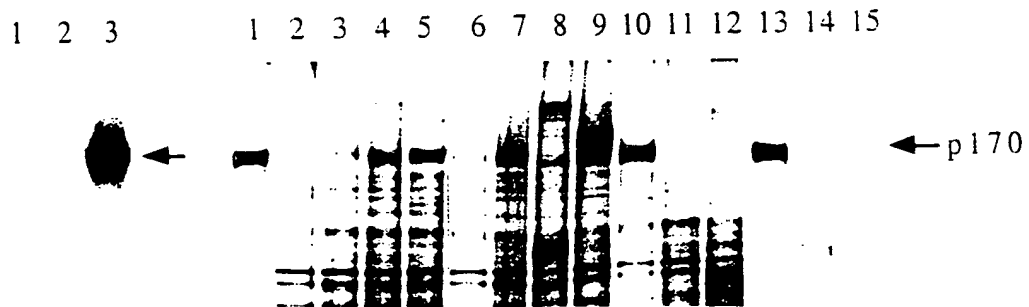


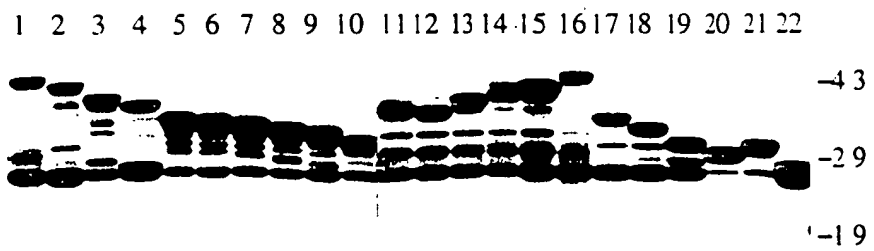


**FIG. 4**

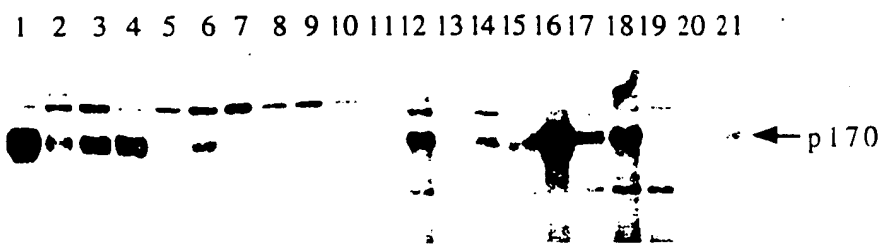


**FIG. 5A**

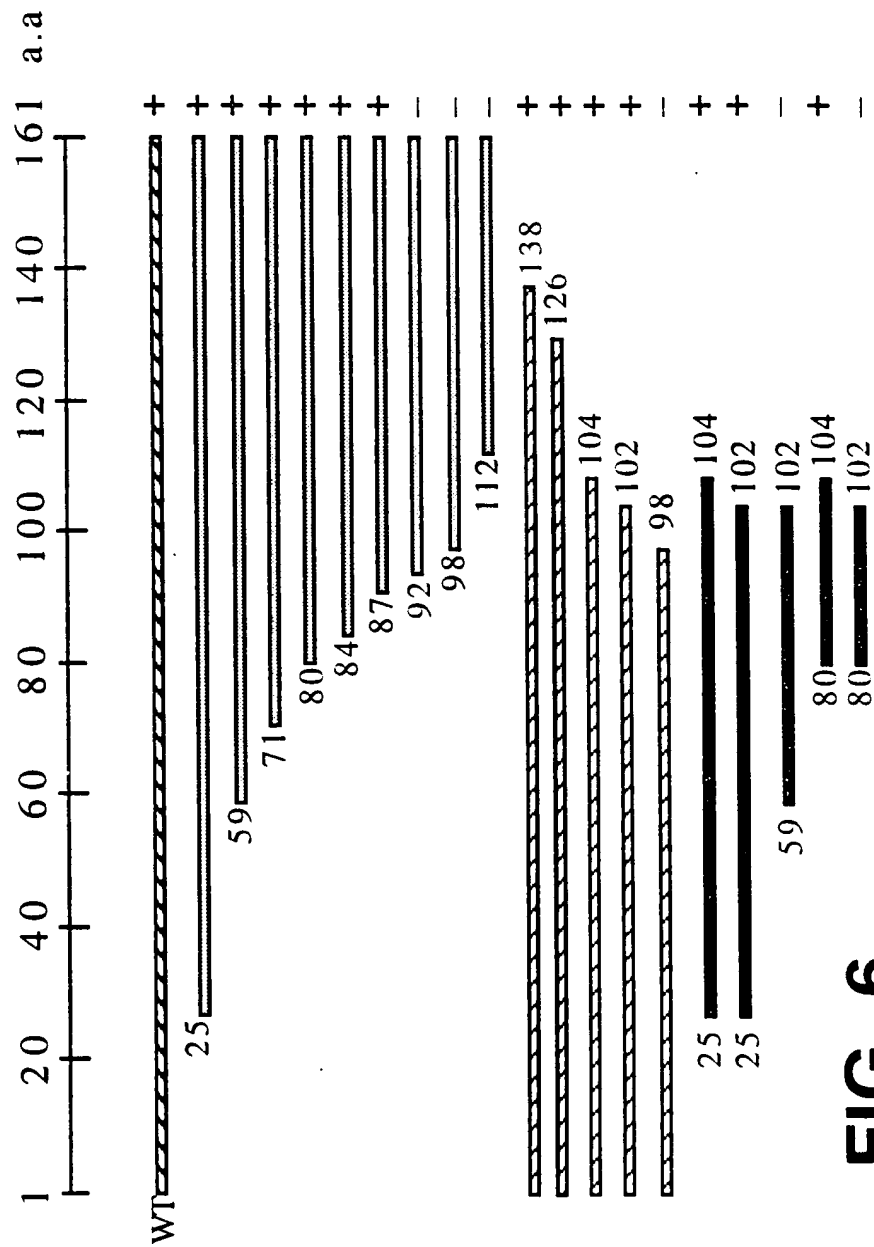
**FIG. 5B**



**FIG. 7A**

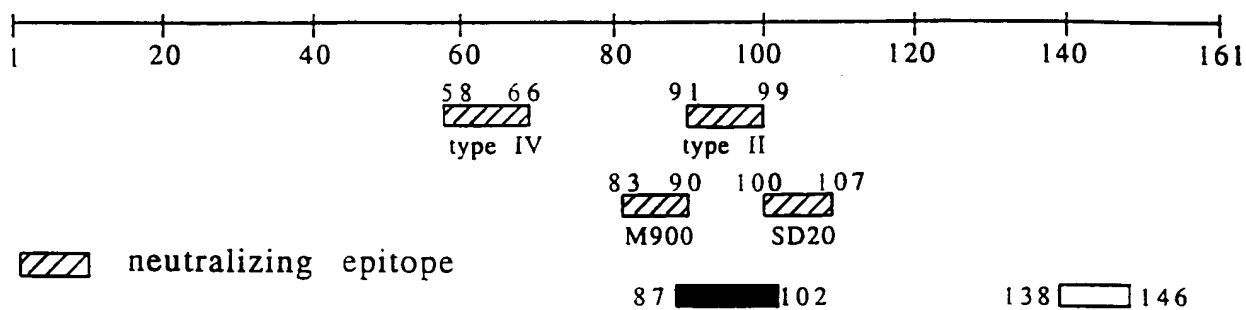


**FIG. 7B**

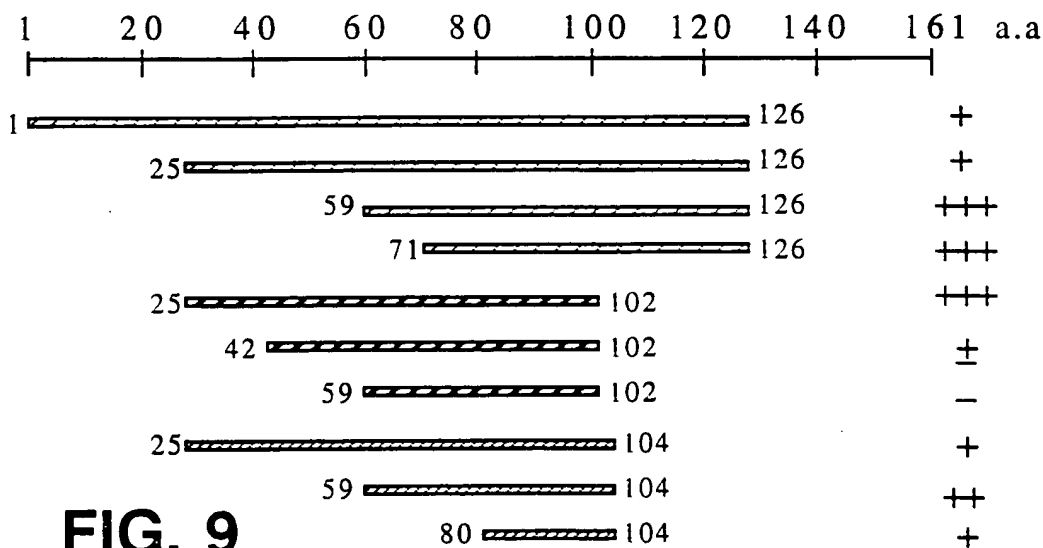


**FIG. 6**

# DHBV pre-S region



**FIG. 8**



**FIG. 9**

1 2 3 4 5 6 7 8 9 10 11

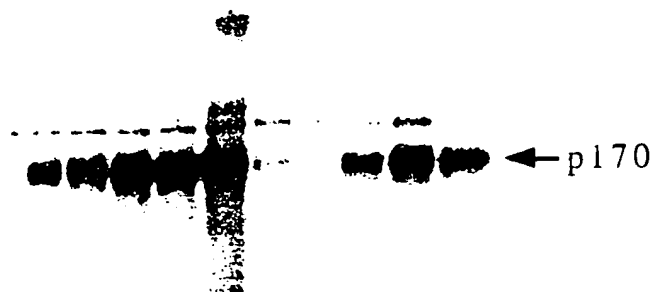


FIG. 10

A pre-S polypeptide containing p170 binding site blocks DHBV infectivity

1 2 3 4



FIG. 11

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16

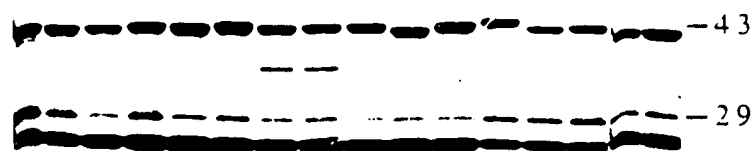


FIG. 13A

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18



FIG. 13B

	87	90	93	96	99	102
wild-type	Q	W	T	P	E	E
W88S	S					
P90L		L				
E91G		G				
E92V			V			
D93F			F			
K95S				S		
R97L					L	
R97C					C	
E98A						A
E98V						V
R102G						G
E91G/K95S		G		S		
E91G/R97C		G			C	
K95S/A96T				S	T	
K95S/R97C				S		C
K95S/R97L/E98A				S	L	A

**FIG. 12**

peptide 1	SVELRELYVMEISDNPGVHEAGEPEFK (SEQ ID NO:19)
peptide 2	LIDRTRIVIVPSLNPDGR-IA (SEQ ID NO:20)
peptide 3	SLLSHEFQDETDTTEEETLYSAK (SEQ ID NO:21)
peptide 4	VEEGKVPVLNTPD (SEQ ID NO:22)

## FIG. 14A

peptide 1	SVELRELYVMEISDNPGVHEAGEPEFK (SEQ ID NO:19)
bovine CPH	.F.G...L.L.L.....P.....
human CPH	.F.G...L.I.L.....P.....
AEBP1 gene	KI.A.....D..L.....R
human CPN	...G.H...L.F..H..I..PL...V.
human CPM	..KG.N.W.LVVGRF.KE.RI.I....

peptide 2	LIDRTRIVIVPSLNPDGR-IA (SEQ ID NO:20)
AEBP1 gene	.VQD...HL.....YEV.
bovine CPH	..HN...H.M.....
human CPN	..QD...H.L..M....YEV.
human CPM	..NS...H.M..M....
human CPH	..HS...H.M.....

## FIG. 14B

	(SEQ	ID NO:)
PK-81		
aa number	6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27	
aa	E L Y V M E I S D N P G V H E A G E P E F K	(23)
possible nt	GAX CTN TAY GTN ATG GAX ATW AGY GAY AAY CCN GGN GTN CAY GAX GCN GGN GAX CCN GAX TTY AAX TTX TCN	(24)
degenerate primer & product	gax ytn tay gtn atg gag atc TCG GAC AAC CCC GGY GTY cay gax ycn ggn gax ccn gax tt	(25) (26)
specific primer & product	atg gag atc tcg gac aac ccc GGC GTC CAT GAA GCA GGT GAG CCA GAG TTC AAG	(27)
PK-69		
aa number	1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22	
aa	S L L S H E F Q D T D T E E E T L Y S A K	(28)
possible nt	AGY CTN CTN AGY CAY GAX TTY CAX GAY ACN GAY ACN GAX GAX GAX GAX GAX GAX GAX GAX GAX GAX GAX GAX GAX TCN TTX TTX TCN	(29)
degenerate primer & product	tz ytn agy cay gax tty cax gat GAA ACA GAC ACT GAA GAA gax acn ytn tay tcn gc v aa	(30) (31)
specific primer & product	TCC CTT TTG AGC CAC GAA TTC CAG Gat gaa aca gac act gaa gaa	(32)

N: G/A/T/C; X: A/G; Y: C/T; Z: G/T; V: A/C; W: A/T/C.

Primer sequences are written in small letters. For convenience antisense primers are written in the sense orientation.

**FIG. 15**



1/1  
 ATG GGG CAA CAT CCA GCA AAA TCA ATG GAC GTC AGA CGG ATA GAA GGA GGA GAA ATA CTG  
 M G Q H P A K S M D V R R I E G G E I L  
 31/11  
 61/21  
 TTA AAC CAA CTT GCC GGA AGG ATG ATC CCA AAA GGG ACT TTG ACA TGG TCA GGC AAG TTT  
 L N Q L A G R M I P K G T L T W S G K F  
 91/31  
 121/41  
 CCA ACA CTA GAT CAC GTG TTA GAC CAT GTG CAA ACA ATG GAG GAG ATA AAC ACC CTC CAG  
 P T L D H V L D H V Q T M E E I N T L Q  
 151/51  
 181/61  
 AAT CAG GGA GCT TGG CCT GCT GCG GGA AGG AGA GTA GGA TTA TCA AAT CCG ACT CCT  
 N Q G A W P A G A G R R V G L S N P T P  
 211/71  
 241/81  
 CAA GAG ATT CCT CAG CCC CAG TGG ACT CCC GAG GAA GAC CAA AAA GCA CGC GAA CCT TTT  
 Q E I P Q P Q W T P E E D Q K A R E A F  
 271/91  
 301/101  
 CGC CGT TAT CAA GAA AGA CCA CCG GAA ACC ACC ATT CCT CCG TCT TCC CCT CCT  
 R R Y Q E E R P P E T T I P P S S P P  
 331/111  
 361/121  
 CAG TGG AAG CTA CAA CCC GGG GAC GAT CCA CTC CTG GGA AAT CAG TCT CTC CTC GAG ACT  
 Q W K L Q P G D D P L L G N Q S L L E T  
 391/131  
 421/141  
 CAT CCG CTA TAC CAG TCA GAA CCA GCG GTG CCA GTG ATA AAA ACT CCC CCC TTG AAG AAG  
 H P L Y Q S E P A V P V I K T P P L K K  
 451/151  
 481/161  
 AAA  
 K

FIG. 16

**FIG. 17A**

**FIG. 17B**

**FIG. 17C**

**FIG. 17D**

**FIG. 17E**

**FIG. 17**

[illegible]

chimpanzee HS1/np08

[illegible]

FIG. 17B

102000 00000000

		Pres2		120		174	
PHBV3200	USA	adw2	A	MOVNSTAFHQTLQDPRVRGLYLPAGGSSGTVNPAPMIASHISSARIGDPVIM			
PHBV933	USA	adw2	A	.....L--A--.....			.....I
PF0U294	the Philippines	adw2	A	.....A--.....f--.....l--v--l--.....s--l--.....AP.			
PMND122	Indonesia	adw2	B	.....l--.....A--f--.....VQ--IV--S--.....LSK--.....P.			
PMTB299	Indonesia	adw2	B	.....l--.....A--f--.....VQ--I--S--.....LST--.....P.			
POOU282	Japan	adw2	B	.....l--.....G--A--f--.....S--Q--IV--A--.....LSK--.....P.			
PJDU233	Japan	adw2	B	.....l--.....A--f--.....S--Q--IV--A--.....LSK--.....P.			
PAK66	Japan	adw	C	.....l--.....A--l--.....f--.....V--II--P--.....IFS--.....AP.			
-K619	Japan	adw	C	.....l--.....A--l--.....f--.....V--II--P--.....FS--.....AP.			
BV1-1	Japan	adr	C	.....l--.....A--l--.....f--.....V--IIV--P--.....FS--.....AP.			
PMRH8adr4	Japan	adr	C	.....l--.....A--l--.....f--.....V--II--P--.....S--.....AP.			
PHBr330	Japan	adr	C	.....l--.....A--l--.....f--.....V--II--P--.....FS--.....AP.			
PADRRho	Korea	adr	C	.....l--.....V--l--.....f--P--.....V--II--P--.....S--.....AP.			
ADRRen	China	adr	C	.....l--.....A--l--.....f--.....V--II--P--.....FS--.....AP.			
PYRB259	Japan	ayr	C	.....l--.....A--l--.....f--.....V--II--P--.....FS--.....AP.			
HMA	New Caledonia	adrq-	C	.....l--O--A--.....V--f--.....V--II--l--.....FS--l--.....			
Cha	Polynesia	adrq-	C	.....l--O--A--l--.....f--.....V--II--l--.....FS--.....			
PHBV320	Latvia	ayw2	D	.....l--.....f--.....V--IIV--P--.....FS--l--.....AL-			
aywut	Italy	ayw2	D	.....l--.....P--.....V--IIV--.....FT--l--.....AL-			
H8Valpha1	Turkey	ayw2	D	.....l--.....f--.....V--IIV--P--.....FS--l--.....AL-			
PPYW310	Papua	ayw2	D	.....l--.....f--.....V--II--P--.....FS--l--.....AL-			
EcoHBVDNA	France	ayw3	D	.....l--.....f--.....VLI--PL--.....FS--l--.....AL-			
PYWB796	Japan	ayw3	D	.....l--.....A--.....f--.....V--II--P--L--.....FSKl--LAP-			
Bas	West Africa	ayw4	E	.....l--.....A--.....f--.....V--II--l--.....FS--l--.....AP-			
kou	Senegal	ayw4	E	.....l--.....A--.....f--.....V--II--l--.....FS--l--.....AP-			
fou	France	adw4	f	.....H--A--l--.....A--f--.....O--.....l--.....SK--G--AH-			
9203/85	Colombia	adw4	f	.....H--A--l--.....A--f--.....O--.....l--.....SK--G--AH-			
adw/LSH	chimpanzee			.....l--.....A--.....f--.....V--l--.....VFSI--.....AP-			

FIG. 17C

[illegible]

**FIG. 17D**

GCAGAGTCIAGACICGCTGGIGGACTTCTCCTCAATTTCTAGGGGAICICCCGTGIGTGCGCCAAATTCGAGTCCCCAACCTCCAATCACACCAACCTCCTGCTCTCCAATTG  
A-----G-----G-A-----C-----  
A-----G-----G-A--AAG-----C-----  
-----G-----G-----G-----G-----  
A-----CIA-----G-----C-----  
A-----C-----CIA--AG-----C-----

13360

**FIG. 17E**

1/1	31/11
ATG GAG ATC TCG GAC AAC CCC GGT GTT CAT	GAA GCA GGT GAG CCA GAG TTC AAG TAT ATT
M E I S D N P G V H	E A G E P E F K Y I
61/21	91/31
GGT AAC ATG CAT GGG AAT GAA GTT GTG GGG	CGA GAG CTG CTC CTG AAC CTC ATC GAG TAC
G N M H G N E V V G	R E L L L N L I E Y
121/41	151/51
CTC TGC AAG AAC TTC GGC ACA GAT CCC GAA	GTG ACT GAC TTG GTC CAG AGC ACG CGG ATC
L C K N F G T D P E	V T D L V Q S T R I
181/61	211/71
CAC ATC ATG CCG TCC ATG AAC CCA GAT GGC	TAC GAG AAG TCC CAG GAA GGA GAC AGA GGA
H I M P S M N P D G	Y E K S Q E G D R G
241/81	271/91
GGC ACC GTT GGC AGA AAT AAC AGC AAC AAC	TAC GAC CTG AAC CGG AAC TTC CCA GAT CAG
G T V G R N N S N N	Y D L N R N F P D Q
301/101	331/111
TTC TTC CAG GTG ACA GAC CCT CCG CAG CCA	GAA ACT CTT GCT GTC ATG AGC TGG TTG AAA
F F Q V T D P P Q P	E T L A V M S W L K
361/121	391/131
ACT TAC CCG TTC GTG CTT TCA GCA AAC CTG	CAT GGA GGT TCT CTG GTG GTT AAT TAC CCT
T Y P F V L S A N L	H G G S L V V N Y P
421/141	451/151
TTT GAT GAC GAT GAA CAA GGA ATA GCC ATA	TAC AGT AAA TCC CCA GAC GAT GCT GTG TTT
F D D D E Q G I A I	Y S K S P D D A V F
481/161	511/171
CAG CAG CTG GCA CTT TCC TAC TCC AAG GAA	AAC AAA AAG ATG TAT CAG GGA AGC CCT TGT
Q Q L A L S Y S K E	N K K M Y Q G S P C
541/181	571/191
AAG GAT TTG TAC CCC ACA GAG TAC TTT CCA	CAT GGC ATC ACG AAC GGG GCC CAG TGG TAC
K D L Y P T E Y F P	H G I T N G A Q W Y
601/201	631/211
AAC GTT CCA GGT GGG ATG CAG GAC TGG AAT	TAC TTA AAT ACC AAC CTG TTT GAA GTG ACC
N V P G G M Q D W N	Y L N T N L F E V T
661/221	691/231
ATT GAG CTG GGC TGT GTG AAA TAC CCA AAA	GCA GAG GAG CTG CCG AAG TAC TGG GAG CAG
I E L G C V K Y P K	A E E L P K Y W E Q
721/241	751/251
AAC CGT AGA TCT CTC CTC CAG TTC ATT AAA	CAG GTT CAC CGC GGC ATC TGG GGA TTT GTG
N R R S L L Q F I K	Q V H R G I W G F V
781/261	811/271
CTG GAT GCC ACG GAC GGA AGG GGC ATT CTC	AAC GCC ACC ATC AGC GTC GCC GAC ATC AAC
L D A T D G R G I L	N A T I S V A D I N
841/281	871/291
CAC CCC GTG ACC ACC TAC AAA GAT GGG GAC	TAC TGG CGC CTC TTG GTC CAG GGG ACG TAC
H P V T T Y K D G D	Y W R L L V Q G T Y
901/301	931/311
AAA GTC ACA GCA TCT GCC CGA GGG TAT GAT	CCA GTC ACT AAA ACG GTG GAA GTC GAC AGC
K V T A S A R G Y D	P V T K T V E V D S
961/321	991/331
AAA GGT GGG GTG CAG GTC AAC TTC ACT CTT	TCA CGG ACA GAC GCC AAA GTG GAG GAG GGG
K G G V Q V N F T L	S R T D A K V E E G
1021/341	1051/351
AAG GTG CCA GTC CTG AAC ACC CCA GAC ACC	AGC GAC CCC AAC GAG AAG GAG TTT GAG ACT
K V P V L N T P D T	S D P N E K E F E T
1081/361	1111/371
CTG ATC AAA GAT CTA TCT GCT GAA AAC GGC	CTG GAG
L I K D L S A E N G	L E

(SEQ ID NO:63)

(SEQ ID NO:64)

**FIG. 18**



1/1	31/11	TTT GTC CAG GAC AAG AGT GGC AAG GCA ATT TCT AAA GCT ACC ATT GTC CTT AAT GAA GGC
61/21	91/31	F V Q D K S G K A I S K A T I V L N E G
121/41	151/51	TTG AGG GTC TAC ACT AAA GAA GGT GGC TAT TTC CAT GTG CTG TTG GCT CCT GGT TTG CAT
181/61	211/71	L R V Y T K E G G Y F H V L L A P G L H
241/81	271/91	AAC ATC AAT GCG ATA GCG GAT GGC TAC CAA AAG CAT ATG AAG GTC TTG GTA CGC CAC
301/101	331/111	N I N A I A D G Y Q Q K H M K V L V R H
361/121	391/131	GAT GCA CCC AGC TCT GTG TTC ATG GTA TTT GAC ATG GAA AAC AGG ATA TTT GGT CTG CCT
421/141	451/151	D A P S S V F M V F D M E N R I F G L P
		CGA GAG CTG GTT GTA ACT GTT GCA GGT GCA ATT ATG TCT GCT TTG GTC CTC ACT GCC TGT
		R E L V V T V A G A I M S A L V L T A C
		ATC ATC TGG TGT GTC TGC TCA ATC AAG GCC AAC AGA CAC AAA GAT GGC TTC CAC TGC CGG
		I I W C V C S I K A N R H K D G F H C R
		CAG CAC CAC GAT TAC GAG GAC GAA ATC CGC ATG ATG TCC ACT GGC TCA AAG AAA TCC
		Q H H D D Y E D E I R M M S T G S K K S
		CTT TTG AGC CAC GAA TTC CAG GAT GAA ACA GAC ACT GAA GAA (SEQ ID NO:65)
		L L S H E F Q D E T D T E E (SEQ ID NO:66)

(SEQ ID NO:65)

HBV (SEQ ID NO:67)  
DHBV (SEQ ID NO:68)

71	H	G	G	I	L	G	W	S	P	Q	A	Q	G	I	L	T	V	S	T	I	P	P	P	A	S	T	N	R	Q	S	G	R	Q	P	T	P	I	S	P	P	L	R	D	S	H	P	Q	118
69	A	G	R	R	V	G	L	S	N	P	T	P	Q	E	I	P	Q	P	Q	W	T	P	E	E	D	Q	K	A	R	E	A	F	R	R	Y	Q	E	E	R	P	P	E	T	T	I	P	P	116
	*		*		*		*		*		*		*		*		*		*		*		*		*		*		*		*		*		*		*		*		*		*		*		*	

HBV (SEQ ID NO:67)  
DHBV (SEQ ID NO:68)

-----  
p170 binding site

FIG. 20

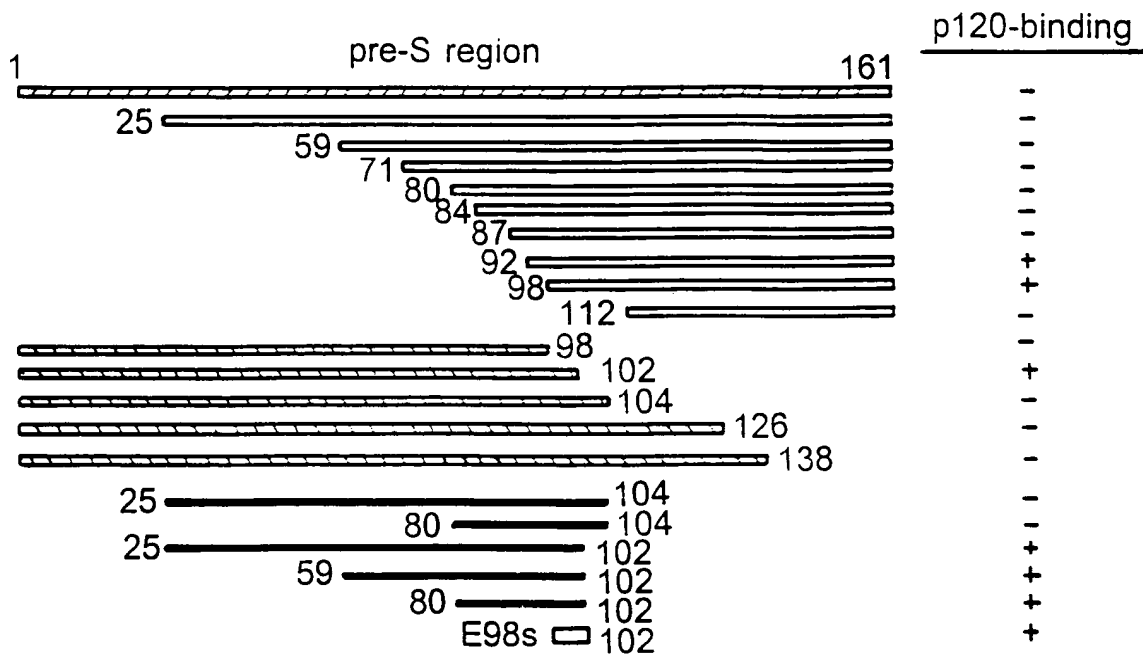


FIG. 21A

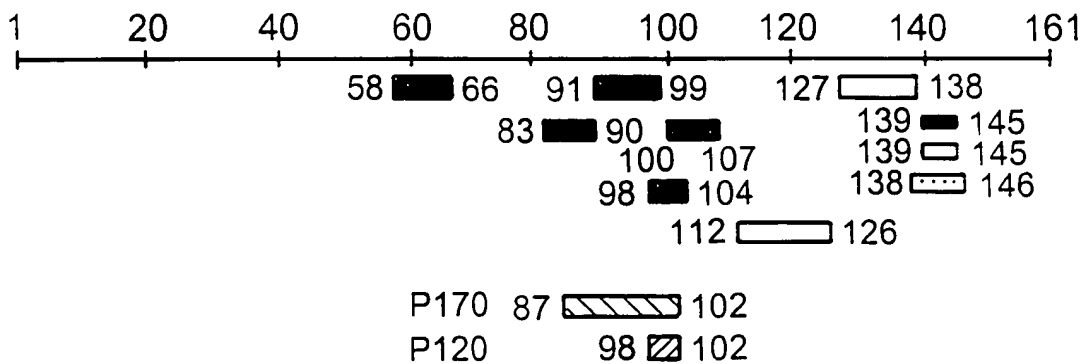


FIG. 22

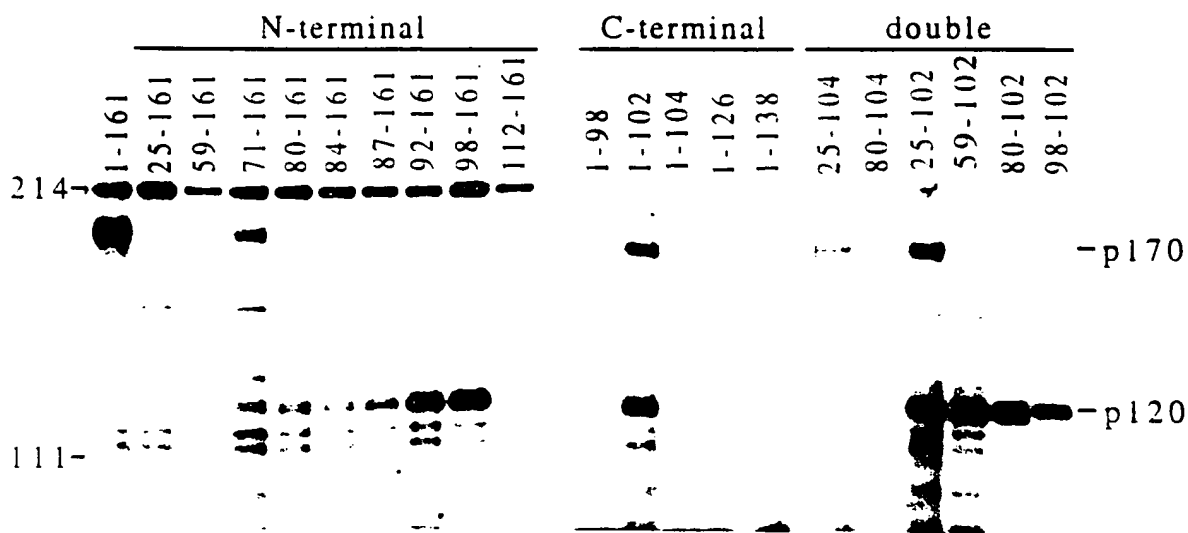


FIG. 21B

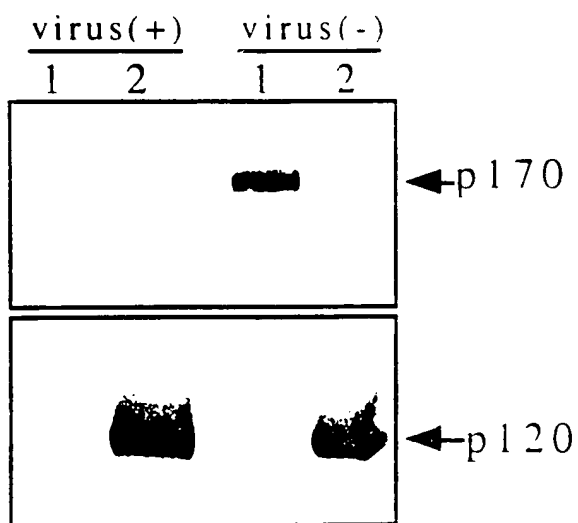


FIG. 23

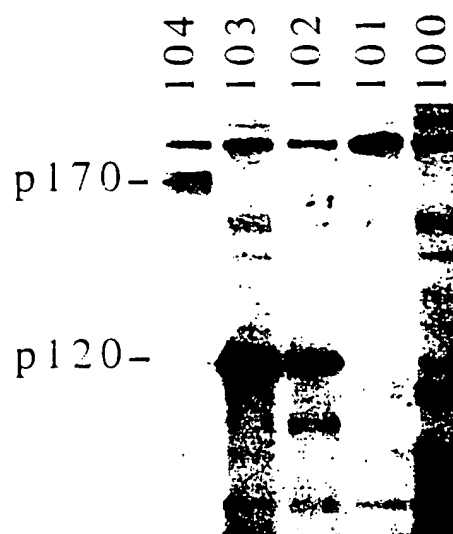


FIG. 24

			97	98	99	100	101	102	<u>p120-binding</u>
WT	Lys	Ala	Arg	Glu	Ala (Tyr)	Phe	Arg	Arg	+
R97C			Cys						+
E98V				Val					+
E98A				Ala					+
A99D					Asp				+
F100V						Val			-
F100L						Leu			-
F100W						Trp			+
R101L							Leu		-
R101H							His		-
R101K							Lys		+ weak
R102G								Gly	-
R102H								His	-
R102K								Lys	-

**FIG. 25A**

peptide 1: DVSGVLFQYPDTEGK (SEQ ID NO:70)

peptide 2: EVYRLALQTREQHRRD (SEQ ID NO:71)

peptide 3: SGAQGEYAGLAAK (SEQ ID NO:72)

peptide 4: IQPIEVDK (SEQ ID NO:73)

Peptide sequences of p120.

**FIG. 30**

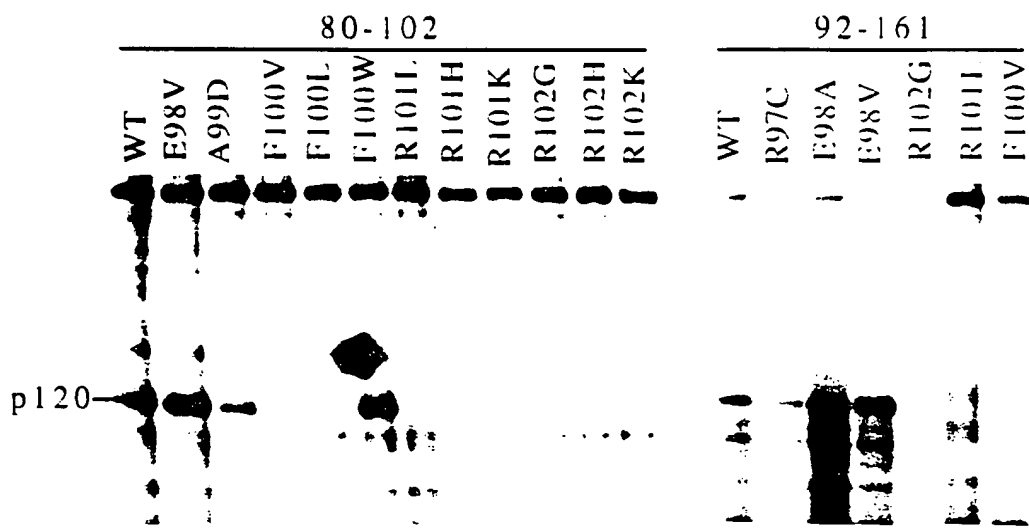


FIG. 25B

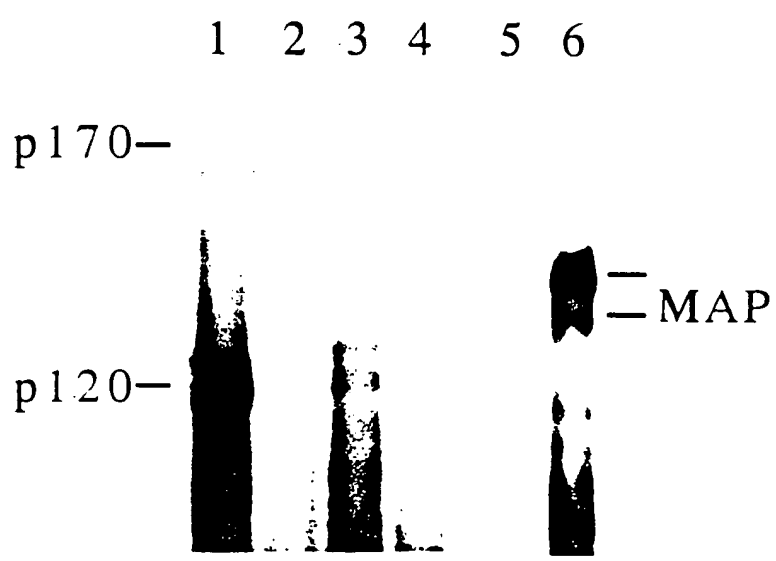


FIG. 26

1 2 3 4 5 6

FIG. 27A

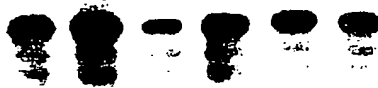


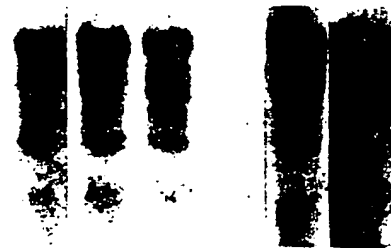
FIG. 27B



FIG. 27C



FIG. 27D



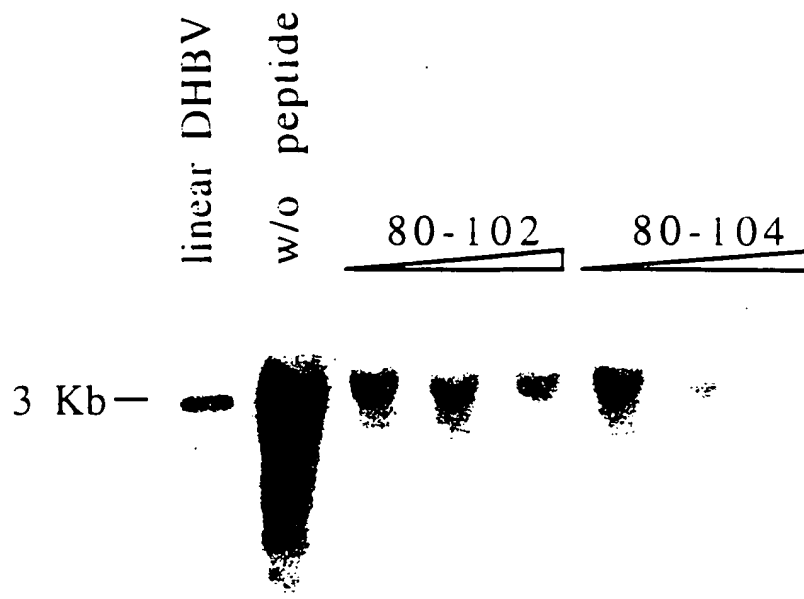


FIG. 28

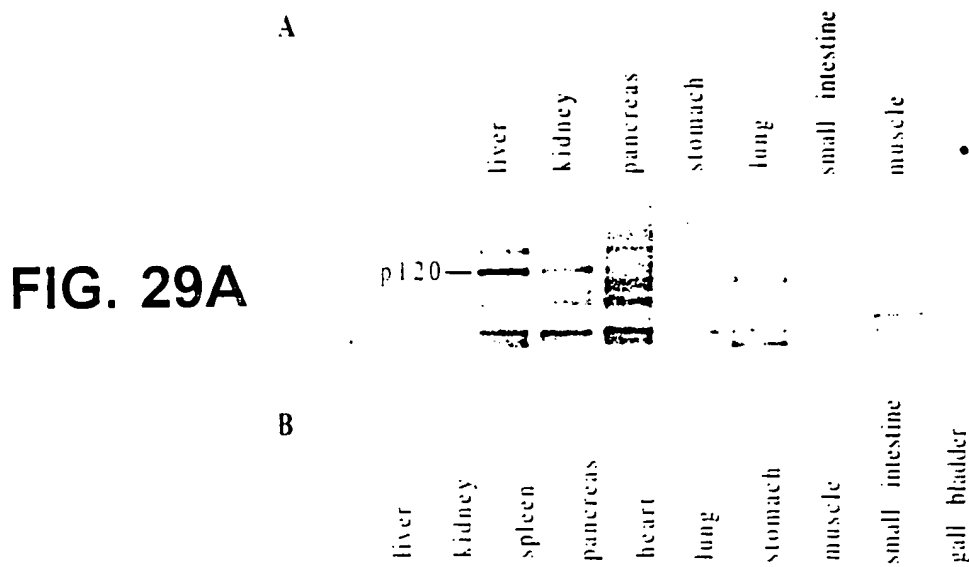


FIG. 29B



1/1  
 GAG CGG CGG TGC ATC GAG CAG CTG CTG CCG CGG CAC GAT TTC TCC CGG CCG CAC  
 E A A R C I E Q L L P R H D D F S R R H  
 61/21  
 ATC GGC CCC CGG GAG GGG GAG AAG AGG GAG ATG CTG CGA GCC CTC GGG GTG CAG AGC GTC  
 I G P R E G E K R E M L R A L G V Q S V  
 121/41  
 GAG GAG CTG ATG GAT AAA GCC ATC CCG GGC AGC AGC CTG GGC AGG CCG CTG AGG ATG  
 E E L M D K A I P G S I R L R R P L R M  
 181/61  
 GAG GAC CCC GTG GGT GAA AAT GAA ATC CTT GAA ACT TTA TAC AAT AAT GCA AGC AAG AAC  
 E D P V G G E N E I L E T L Y N I A S K N  
 241/81  
 AAG ATA TGG AGG TCC TAT ATA GGC ATG GGT TAT TAC AAC TGC TCA GTG CCT CAA CCC ATT  
 K I W R S Y I G M G Y Y N C S V P Q P I  
 301/101  
 GCA CGG AAT TTG TTG GAG AAT GCA GGA TGG GTT ACC CAG TAT ACT CCC TAC CAA CCT GAG  
 A R N L L E N A G W V T Q Y T P Y Q P E  
 361/121  
 GTC TCA CAG GGC AGG CTG GAG AGC CTG CTA AAT TAC CAG ACT ATG GTG TGT GAT ATC ACA  
 V S Q G R L E S L L N Y Q T M V C D I T  
 421/141  
 CGA ATG GAT GTG GCT AAT GCA TCA TTG CTG GAT GAG GGG ACA GCT GCT GCA GAA GCT ATG  
 G M D V A N A S L L D E G T A A A E A M  
 481/161  
 CAA TTA TGT CAC AGG CAC AAC AAA AGG AGG AAG TTT TAT GTA GAT TCC CGA TGC CAC CCT  
 Q L C H R H N K R R K F Y V D S R C H P

FIG. 31A

541/181 571/191  
 CAG ACT ATA GCA GTG GTC CAA ACT AGA GCC AAT TAT ACA GGT GTT ATT ACT GAG CTC AAA  
 Q T I A V V Q T R A N Y T G V I T E L K  
 601/201 631/211  
 TTA CCC CAT GAG ATG GAT TTC AGT GGA AAG GAT GTC AGT GGA GTA TTA TTT CAG TAT CCA  
 L P H E M D F S G K D V S G V L F Q Y P  
 661/221 691/231  
 GAC ACT GAG GGG AAG GTG GAA GAC TTC TCT GAA CTT GTT GAA AGA GCT CAT CAG AAC GGG  
 D T E G K V E D F S E L V E R A H Q N G  
 721/241 751/251  
 ACT CTT GCC TGC TGT GCT ACT GAT CTT CTG GCT CTC TGT ATT CTG AAG CCT CCT GGA GAG  
 T L A C C A T D L L A L C I L K P P G E  
 781/261 811/271  
 TTT GGG GTA GAT GTT GTC CTG GGT AGC TCC CAG AGA TTT GGT GTG CCA CTC TGC TAT GGG  
 F G V D V V L G S S Q R F G V P L C Y G  
 841/281 871/291  
 GGA CCC CAC GCA GCA TTC TTT GCT GTC AAG GAA AAC CTA GTG AGA ATG ATG CCA GGC AGG  
 G P H A A F F A V K E N L V R M M P G R  
 901/301 931/311  
 ATG GTG GGT GTC ACA AGA GAT GCA AAT GGA AAA GAA GTT TAC CGA CTG GCT TTA CAA ACA  
 M V G V T R D A N G K E V Y R L A L Q T

FIG. 31B

961/321 CGA GAG CAG CAT ATC AGG AGG GAC AAA GCT ACA AGC AAC ATC TGC ACA GCA CAG GCT CTT  
 R E Q H I R R D K A T S N I C T A Q A L  
 1021/341 1051/351  
 CTC GCT AAT ATG GCA GCC ATG TTT GGT GTC TAC CAT GCG TCT GAT GGA TTA AGG GAT ATT  
 L A N M A A M F G V Y H G S D G L R D I  
 1081/361 1111/371  
 GCA AGA CCG GTA CAC AAT GCT ACT TTA ATC CTG GCT GAA GGT CTC AGG AGA GCT GGT CAT  
 A R R V H N A T L I L A E G L R A G H  
 1141/381 1171/391  
 AAA CTG CAC CAT GAT CTG TTC TTT GAT ACC TTG ACA GTC ACG TGT GGA TGC TCA GTC AAA  
 K L H H D L F F D T L T V T C G C S V K  
 1201/401 1231/411  
 GAA GTT TTG GAC AGG GCA GCT CTG AGA AAG ATA AAT TTT CGC ATT TAT AGT GAT GCC AGA  
 E V L D R A A L R K I N F R I Y S D G R  
 1261/421 1291/431  
 CTT GCA GTA TCA CTT GAT GAA ACT GTA AGT GAG AAA GAC CTA GAT GAC ATA TTA TGG ATT  
 L G V S L D E T V S E K D L D D I L W I  
 1321/441 1351/451  
 TTT GGT TGC GAG TCT TCA GCT GAA CTA ATT GCT GAA GGT ATG GGC GAG GAA ACC AAA GGT  
 F G C E S S A E L I A E G M G E E T K G  
 1381/461 1411/471  
 ATC CTT AGC ACC CCA TTT AAG AGA ACT TCC AAA TTC TTG ACC CAT CAG GTT TTC AAC AGC  
 I L S T P F K R T S K F L T H Q V F N S

FIG. 31C

1441/481  
 TAT CAC TCC GAA ACA AAT ATC GTA CGG TAC ATG AAG AGA TTA GAA AAC AAA GAT ATT TCC  
 Y H S E T N I V R Y M K R L E N K D I S  
 1501/501  
 CTT GTT CAC AGC ATG ATT CCT TTG GGG TCC TGT ACA ATG AAG CTC AAT AGT TCA GCT GAA  
 L V H S M I P L G S C T M K L N S S A E  
 1561/521  
 CTT GCA CCT ATT TCA TGG AAG GAA TTT GCC AAC ATC CAC CCC TTT GTG CCC TTG GAT CAA  
 L A P I S W K E F A N I H P F V P L D Q  
 1621/541  
 GCT CAA GGG TAT CAG CAG CTT TTC AAG GAC TTA GAG AAG GAC CTG TGT GAG ATT ACT GGT  
 A Q G Y Q Q L F K D L E K D L C E I T G  
 1681/561  
 TAC GAC AAA ATC TCC TTC CAA CCA AAC AGT GGA GCC CAA GGA GAG TAC GCA GGC TTG GCC  
 Y D K I S F Q P N S G A Q G E Y A G L A  
 1741/581  
 GCA ATC AAA GCT TAT TTA AAT GCA AAA GGA GAA CGT CAT CGA AGT GTT TGC CTT ATT CCT  
 A I K A Y L N A K G E R H R S V C L I P  
 1801/601  
 AGA TCT GCT CAT GGT ACA AAT CCA GCA AGT GCA CAG ATG GCA GGG ATG AAG ATT CAA CCA  
 R S A H G T N P A S A Q M A G M K I Q P

FIG. 31D

1861/621  
GTT GAA GTA GAT AAA AAT GGG AGC ATT GAT ATC TCC CAT TTA AAA GCA ATG GTG GAC AAA  
V E V D K N G S I D I S H L K A M V D K

1921/641  
CAC AAG GAG AAC CTG GCA GCC ATC ATG ATC ACA TAC CCT TCC ACC AAT GGT GTG TTT GAG  
H K E N L A A I M I T Y P S T N G V F E

1891/631  
GAG GAG ATT GGG GAT GTG TGT GAG CTG ATT CAC AAA AAC GGA GGC CAG GTT TAC CTG GAT  
E E I G D V C E L I H K N G G Q V Y L D

2041/681  
GGA GCA AAC ATG AAC GCC CAA GTG GGT CTG TGT CGT CCT GGA GAT TAT GGC TCT GAT GTC  
G A N M N A Q V G L C R P G D Y G S D V

2101/701  
TCT CAC TTA AAC CTT CAC AAA ACC TTT TGC ATT CCC CAT GGA GGA GGA CCT GGA ATG  
S H L N L H K T F C I P H G G G P G M

2161/721  
GGA CCA ATT GGA GTG AAG AAA CAT CTG GCT CCC TAC TTG CCT ACC CAT CCT GTC ATC AAG  
G P I G V K K H L A P Y L P T H P V I K

2011/671  
GAG GAG ATT GGG GAT GTG TGT GAG CTG ATT CAC AAA AAC GGA GGC CAG GTT TAC CTG GAT  
E E I G D V C E L I H K N G G Q V Y L D

2071/691  
GGA GCA AAC ATG AAC GCC CAA GTG GGT CTG TGT CGT CCT GGA GAT TAT GGC TCT GAT GTC  
G A N M N A Q V G L C R P G D Y G S D V

2131/711  
TCT CAC TTA AAC CTT CAC AAA ACC TTT TGC ATT CCC CAT GGA GGA GGA CCT GGA ATG  
S H L N L H K T F C I P H G G G P G M

2191/731  
GGA CCA ATT GGA GTG AAG AAA CAT CTG GCT CCC TAC TTG CCT ACC CAT CCT GTC ATC AAG  
G P I G V K K H L A P Y L P T H P V I K

FIG. 31E

2221/741  
ATT CAG ACG GAT AAG GAT GCA TGT CCT TTG GGT ACT GTC AGT GCT GCA CCT TGG GGT TCC  
I Q T D K D A C P L G T V S A A P W G S

2281/761  
AGT GCT ATA TTG CCT ATT TCC TGG GTG TAT ATC AAG ACA ATG CGA GCA AAG GGT CTT AAA  
S A I L P I S W V Y I K T M G A K G L K

2341/781  
CAC GCT TCT GAG GTT GCT ATA TTA AAT GCA AAC TAC ATG GCA AAG AGG CTG GAG AAG CAC  
H A S E V A I L N A N Y M A K R L E K H

2401/801  
TAC AAA ATC CTT TTC AGA GGA GTA AGA GGT TAT GTA GCC CAT GAA TTC ATT TTG GAT ACA  
Y K I L F R G V R G Y V A H E F I L D T

2461/821  
AGA CCT TTC AAA ACA GCA AAC ATT GAA GCT GTG GAT CTT GCT AAG CGA CTT CAG GAT  
R P F K K T A N I E A V D L A K R L Q D

2521/841  
TAT GGT TTT CAT GCT CCA ACC ATG TCC TGG CCA GTG GCA GCC ACA CTT ATG ATT GAA CCA  
Y G F H A P T M S W P V A G T L M I E P

2581/861  
ACA GAG TCT GAA GAC AAG GCA GAG CTG GAC AGG TTT TGT GAT GCA ATG ATC AGT ATT CGA  
T E S E D K A E L D R F C D A M I S I R

2251/751  
2311/771  
2371/791  
2431/811  
2491/831  
2551/851  
2611/871

FIG. 31F

2641/881  
 CAG GAA ATT GCT GAA ATA GAG GAG GGC AGG ATG GAC CCT CAG ATT AAC CCA TTA AAG ATG  
 Q E I A E I E E G R M D P Q I N P L K M  
 2701/901  
 TCA CCA CAT ACT CTA AAC TGT GTC ACT TCT TCA AAG TGG GAT CGT CCT TAT TCC AGA GAA  
 S P H T L N C V T S S K W D R P Y S R E  
 2761/921  
 GTG GCA GCA TTC CCA CTG CCG TTT GTG AAA CCT GAG AGC AAG TTT TGG CCC ACA ATT GCT  
 V A A F P L P F V K P E S K F W P T I A  
 2821/941  
 CGC ATC GAT GAC ATA TAC GGA GAT CAA CAC CTG GTT TGT ACC TGC CCA CCG ATG GAA GCC  
 R I D D I Y G D Q H L V C T C P P M E A  
 2881/961  
 TAC GAA TCT CCC TTC TCT GAA CAG AAG AGA GCA TCT TCG TAA (SEQ ID NO:74)  
 Y E S P F S E Q K R A S S \* (SEQ ID NO:75)

FIG. 31G